AMENDMENTS TO THE CLAIMS

Please amend claim 68 as shown below.

1-44. **(Canceled)**

45. **(Previously Presented)** A method of detecting an amplification or gain of unique sequences at at least one chromosomal region selected from the group consisting of:

on human chromosome 1,
about position p22 to the centromere;
the q arm;
the centromere to about position p32;
about position q31 to qter;
about position q32;
about position q32 to qter;
on human chromosome 2,
the p arm;
on human chromosome 3,
about position p14;
about position p14 to qter;
about position p22 to pter;
about position q26 to qter;
on human chromosome 4,
the p arm;
about position q32 to about position q34;
on human chromosome 5,
the p arm;
about position q31 to qter;
about position q32 to qter;
on human chromosome 6,

the p arm;

the centromere to about position p21;

about position p23 to pter;

the centromere to about position q21;

about position q12 to about position q13;

about position q21;

about position q21 to about position q22;

on human chromosome 7,

the p arm;

the centromere to about position p12;

about position p21;

pter to about position q31;

the q arm;

about position q22 to about position q32;

on human chromosome 8,

about position p12;

the q arm;

about position q21;

about position q21 to about position q23;

about position q21 to qter;

about position q22 to about position q23;

about position q22 to qter;

about position q23 to about position q24;

about position q23 to qter;

about position q24;

on human chromosome 10,

the p arm;

the centromere to about position q21;

about position q22;

on chromosome 11,

about position p15;

the q arm;

about position q13;

on human chromosome 12,

the p arm;

the q arm;

about position q14 to about position q15;

about position q21;

about position q21 to about position q23;

about position q24;

on human chromosome 13,

about position 22 to qter;

about position q31 to qter;

on human chromosome 14,

the q arm;

about position q24 to qter;

about position q31;

about position q31 to qter;

on human chromosome 15,

about position q21 to qter;

about position q24;

about position q25;

about position q26;

entire human chromosome 16;

on human chromosome 16,

the p arm;

the q arm;

about position q23 to about position q24;

on human chromosome 17,

the centromere to about position q24;

about position q12;

about position q21 to qter;

about position q22 to about position q23;
about position q22 to about position q24;
about position q22 to qter;
about position q24 to qter;
on human chromosome 18,
the p arm;
on human chromosome 19,
the q arm;
about position q13;
about position q13 to qter;
entire human chromosome 20;
on human chromosome 20,
the p arm;
the q arm;
about position q12 to about position q13;
about position q13;
about position q13 to qter;
about position q34;
qter;
entire chromosome 21;
entire chromosome 22;
on the human X chromosome,
the p arm,
in a test sample, said method comprising:

(a) labelling nucleic acids from the test sample and from a control sample with different labels;

(b) contacting said labelled nucleic acids from each sample with a plurality of target nucleic acids, wherein either the labelled nucleic acids or the target nucleic acids, or both, have had repetitive sequences, if initially present, blocked and/or removed; and

(c) comparing the intensities of the signals from labelled nucleic acids hybridized to each

target nucleic acid, thereby allowing detection of the presence or absence of the gain or amplification in the test sample.

46. **(Previously Presented)** The method of claim 45, wherein the step of comparing the intensities of the signals from the labelled nucleic acids comprises determining the ratio of the intensities of the signals as a function of position in the target nucleic acids.

47. **(Previously Presented)** The method of claim 45, wherein the amplification is of the q arm of human chromosome 1.

48. **(Previously Presented)** The method of claim 45, wherein the amplification is of the p arm of human chromosome 7.

49. **(Previously Presented)** The method of claim 45, wherein the amplification is of the q arm of human chromosome 8.

50. **(Previously Presented)** The method of claim 45, wherein the amplification is at about position q24 on human chromosome 8.

51. **(Previously Presented)** The method of claim 45, wherein the amplification is of the q arm of human chromosome 11.

52. **(Previously Presented)** The method of claim 45, wherein the amplification is at about position q13 on human chromosome 11.

53. **(Previously Presented)** The method of claim 45, wherein the amplification is of the q arm of human chromosome 12.

54. **(Previously Presented)** The method of claim 45, wherein the amplification is of the q arm of human chromosome 14.

55. **(Previously Presented)** The method of claim 45, wherein the amplification is of the q arm of human chromosome 16.

56. **(Previously Presented)** The method of claim 45, wherein the amplification is at about position q22 to about position q24 on human chromosome 17.

57. **(Previously Presented)** The method of claim 45, wherein the amplification is of the q arm of human chromosome 20.

58. **(Previously Presented)** The method of claim 45, wherein the target nucleic acids comprise at least one metaphase chromosome.

59. **(Previously Presented)** The method of claim 45, wherein said nucleic acid sample comprises genomic DNA molecules.

60. **(Previously Presented)** The method of claim 45, wherein said nucleic acid sample comprises DNA amplified from said test sample.

61. **(Previously Presented)** The method of claim 45, wherein said nucleic acid sample comprises complementary DNA.

62. **(Previously Presented)** A method of detecting a deletion of unique sequences at at least one chromosomal region selected from the group consisting of:

on human chromosome 9, the p arm;
on human chromosome 16,
the q arm;
about position q22;
on human chromosome 17, the p arm;
in a test sample, said method comprising:

(a) labelling nucleic acids from the test sample and from a control sample with different labels;

(b) contacting said labelled nucleic acids from each sample with a plurality of target nucleic acids, wherein either the labelled nucleic acids or the target nucleic acids, or both, have had repetitive sequences, if initially present, blocked and/or removed; and

(c) comparing the intensities of the signals from labelled nucleic acids hybridized to each

target nucleic acid, thereby allowing detection of the presence or absence of the deletion in the test sample.

63. **(Previously Presented)** The method of claim 62, wherein the step of comparing the intensities of the signals from the labelled nucleic acids comprises determining the ratio of the intensities of the signals as a function of position in the target nucleic acids.

64. **(Previously Presented)** The method of claim 62, wherein the target nucleic acids comprise at least one metaphase chromosome.

65. **(Previously Presented)** The method of claim 62, wherein said nucleic acid sample comprises genomic DNA molecules.

66. **(Previously Presented)** The method of claim 62, wherein said nucleic acid sample comprises DNA amplified from said test sample.

67. **(Previously Presented)** The method of claim 62, wherein said nucleic acid sample comprises complementary DNA.

68. **(Currently Amended)** A method for detecting a copy number variation in a suspected breast cancer sample by detecting an amplification of unique sequences <u>from</u> [[at]] at least one chromosomal region, wherein said chromosomal region is on chromosome 17, position q22 to position q24,

said method comprising:

(a) contacting a probe that binds selectively to a target polynucleotide sequence of said region with a nucleic acid sample prepared, directly or indirectly, from said suspected breast cancer sample, wherein said nucleic acid sample comprises said target polynucleotide sequence and said probe is contacted with said sample under conditions in which said probe forms a stable hybridization complex with said target nucleic acid sequence; and

(b) detecting said hybridization complex.

69. **(Previously Presented)** The method of claim 68, wherein said probe is labeled.

70. **(Previously Presented)** The method of claim 68, wherein said nucleic acid sample is labeled.

71-73. **(Canceled)**

74. **(Previously Presented)** The method of claim 68, wherein said nucleic acid sample comprises genomic DNA molecules.

75. **(Previously Presented)** The method of claim 68, wherein said nucleic acid sample comprises DNA amplified from said suspected breast cancer sample.

76. **(Previously Presented)** The method of claim 68, wherein said nucleic acid sample comprises complementary DNA.

77-86. **(Canceled)**